Biogeosciences

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Supplement of

Merging bio-optical data from Biogeochemical-Argo floats and models in marine biogeochemistry

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Contents

1 Methods: Correction of PAR

In order to derive scalar irradiance from measured downward irradiance we considered the formula from the report: *CSIRO Environmental Modelling Suite: Scientific description of the optical, carbon chemistry and biogeochemical models.* Published by the CSIRO Coastal Environmental Modelling Team in date October 16, 2015 this report describes the software used in Baird et al. (2016). In their equation (16), pg 22 of the report, they derive a formula to express the scalar irradiance (E_o) in terms of downward irradiance (E_d):

$$E_{o,\lambda} = \frac{E_{d,\lambda}}{cos\theta_{sw}} \sqrt{1 + (g_i + g_{ii}cos\theta_{sw})\frac{b_{T,\lambda}}{a_{T,\lambda}}} \qquad (1)$$

where θ_{sw} is the azimuth angle of the mean light path through the water. In our case we neglected the term related to scattering $[(g_i + g_{ii}cos\theta_{sw})\frac{b_{T,\lambda}}{a_{T,\lambda}}]$ because it was not straightforward to derive it from BGC-Argo float measurements.

2 Methods: WMO CODES chart

	LOV NAME	WMO CODE	DATE START	DATE END	LON START	LAT START	LON END	LAT END
1	lovbio001i	6901032	2012-11-26	2013-01-24	7.9129	43.3976	6.3333	42.5095
2	lovbio015c	6901513	2013-05-11	2015-03-18	5.5448	38.3756	6.8693	39.2280
3	lovbio016c	6901510	2013-05-28	2015-05-26	18.5325	37.7258	20.1217	36.7031
4	lovbio016d	6902700	2015-11-08	2016-01-04	8.5423	43.7651	8.1138	43.1795
5	lovbio017b	6901512	2013-04-11	2014-05-04	5.0089	41.9508	3.5216	41.4342
6	lovbio018c	6901528	2013-05-18	2015-05-23	28.0316	33.5997	31.4002	32.3531
7	lovbio035b	6901511	2013-02-21	2014-09-05	4.8633	42.2572	-2.1469	36.2265
8	lovbio039b	6901483	2013-07-25	2014-03-21	12.3115	38.9780	13.0921	38.4307
9	lovbio042c	6901490	2013-06-21	2013-07-07	11.9805	39.6628	11.9365	39.3841
10	lovbio053b	6901529	2013-05-29	2015-02-05	18.5210	37.7431	17.2169	40.0952
11	lovbio058c	6901491	2013-06-18	2015-05-20	11.9656	39.7163	11.2266	39.3356
12	lovbio063c	6901653	2015-03-03	2015-12-22	2.9287	40.9927	4.1317	39.4429
13	lovbio064b	6901496	2013-07-21	2014-03-13	7.8108	43.2953	7.7282	43.2507
14	lovbio064c	6901776	2014-03-17	2014-09-07	7.4037	43.1240	7.3871	42.9534
15	lovbio066c	6901605	2014-02-13	2014-05-22	20.5494	37.0316	22.2422	36.5036
16	lovbio066d	6901655	2014-08-04	2015-05-20	28.5970	34.6950	28.4608	33.5665
17	lovbio067c	6901649	2014-07-17	2016-01-05	5.9916	40.7025	4.4168	41.5186
18	lovbio068d	6901648	2014-07-11	2016-01-01	4.6018	41.9309	4.5600	41.0035
19	lovbio072c	6901600	2014-08-24	2015-09-10	6.5453	37.7768	3.0177	38.1262
20	lovbio083d	6901764	2015-07-01	2015-12-18	27.0414	34.6217	27.8136	33.9370
21	lovbio085d	6901766	2015-05-27	2016-01-03	27.1585	34.5837	27.8724	34.5843
22	lovbio088d	6901768	2015-05-20	2015-11-28	18.5157	38.3012	18.0528	37.5547
23	lovbio089d	6901769	2015-06-04	2015-12-12	10.6694	39.2940	10.1485	39.2201
24	lovbio090d	6901770	2015-05-23	2015-12-18	27.8026	35.6123	26.8293	35.0650
25	lovbio091d	6901771	2015-06-01	2016-01-01	20.0461	36.7235	19.5772	35.9591
26	lovbio093d	6901773	2015-05-27	2015-12-24	28.2032	33.4612	29.4236	33.1930
27	ogsbio001b	6901861	2014-05-28	2015-02-17	36.9278	1.3854	36.5892	
28	ogsbio002b	6901864	2015-06-02	2016-01-02	10.7674	39.2503	8.4489	38.3500
29	ogsbio003b	6901862	2015-03-29	2015-12-28	18.3117	41.5346	18.1775	39.5091
30	ogsbio004b	6901863	2015-05-30	2016-01-02	20.0672	36.6967	19.0187	36.4012
31	ogsbio006b	6901865	2014-02-21	2015-03-20	17.7034	41.8324	17.4001	38.5404

3 Methods: BFM Configuration parameters

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#-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-
# NAMELISTS
#-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-
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# BFM - Biogeochemical Flux Model
#-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-
#
# COPYING
#
#   Copyright (C) 2015 BFM System Team (bfm_st@lists.cmcc.it)
#
#   This program is free software; you can redistribute it and/or modify
#   it under the terms of the GNU General Public License as published by
#   the Free Software Foundation;
#   This program is distributed in the hope that it will be useful,
#   but WITHOUT ANY WARRANTY; without even the implied warranty of
#   MERCHANTEABILITY or FITNESS FOR A PARTICULAR PURPOSE.  See the
#   GNU General Public License for more details.
#
#------------------------------------------------------------------------!


%!------------------------------------------------------------------------!
%!NAMELIST bfm_nml
%!------------------------------------------------------------------------!
%! Main initialisation and output specifications
%! NAME          KIND     DESCRIPTION
%! bio_calc      logical Switch on/off BFM (for coupled configurations)
%! bfm_init      integer Initialization state
%!                        0. from constant values in bfm_init_nml below
%!                        1. from restart
%! bfm_rstctl    logical Save initial state of bfm in the output file.
%! bio_setup     integer BFM configuration:
%!                        1. pelagic
%!                        2. benthic
%!                        3. pelagic and benthic
%!                        4. sea ice
%!                        5. pelagic and sea ice
%! out_fname     string  Name of NetCDF output file
%! out_dir       string  Path to the output file
%! out_title     string  Name of the experiment in NetCDF file
%! out_delta     integer Output is saved every out_delta timesteps
%!                        Use -1 to store with real monthly frequency
%! parallel_log  logical Set true in parallel jobs for a single log file
%!------------------------------------------------------------------------!
%&bfm_nml
%   bio_calc     = .TRUE.
%   bfm_init     = 0
%   bfm_rstctl   = .FALSE.
%   bio_setup    = 1
%   out_fname    = 'BFM_standalone_pelagic'
%   out_dir      = '.'
%   out_title    = 'BFM_STANDALONE_PELAGIC'
%   in_rst_fname = 'in_bfm_restart'
%   out_delta    = 300  !every 30 days
%   parallel_log = .FALSE.
% filename_nml_conf = 'BFM_General.nml',
%/
%


!------------------------------------------------------------------------!
! NAMELIST Param_parameters
!------------------------------------------------------------------------!
! Global Switches : turn on/off or choose model components
! NAME                     KIND    DESCRIPTION
! CalcPelagicFlag          logical Pelagic System
! CalcBenthicFlag          numeric Benthic system
!                                  0 = No Benthic System
!                                  The following are Not Yet Activated
!                                  1 = Simple Benthic Return
!                                  2 = Benthic organisms and intermediate
!                                      complexity nutrient regeneration
!                                  3 = Benthic organisms and full nutrient
!                                      regeneration (early diagenesis)
! CalcTransportFlag        logical Compute Transport Term (when coupled
!                                  with a OGCM)
! CalcConservationFlag     logical Mass Conservation Check
! CalcPhytoPlankton        logical Pelagic Phytoplankton (vector)
! CalcPelBacteria          logical Pelagic Bacteria (vector)
! CalcMesoZooPlankton      logical Mesozooplankton (vector)
! CalcMicroZooPlankton     logical Microzooplankton (vector)
! CalcPelChemistry         logical Pelagic Hydrochemical Processes
! AssignPelBenFluxesInBFMFlag logical Benthic-pelagic fluxes are added to the
!                                  time integration
! AssignAirPelFluxesInBFMFlag logical Air-sea fluxes are added to the
!                                  time integration
! ChlDynamicsFlag    numeric Choose the dynamics of Chl-a
!                            1 = diagnostic, optimal light property
!                                in phytoplankton
!                                (Ebenhoeh et al 1995, ERSEM-II)
!                            2 = state variable, constituent of
!                                phytoplankton
! check_fixed_quota        numeric Check whether zooplankton have fixed quota
!
! Global Parameters : used throughout the model and not related
!                to a specific component
! NAME          UNIT         DESCRIPTION
! p_small       [-]          Smallest numeric value (the model "zero")
! slp0          [mbar]       Reference sea level pressure
! p_pe_R1c      [-]          Fractional content of C in cytoplasm
! p_pe_R1n      [-]          Fractional content of N in cytoplasm
! p_pe_R1p      [-]          Fractional content of P in cytoplasm
! p_qro         [mmolHS-/    Stoichiometric coefficient for
!               mmolO2]      anaerobic reactions
! p_qon_dentri [mmolO2/      Stoichiometric coefficient for
!               mmolN]       denitrification
! p_qon_nitri  [mmolO2/      Stoichiometric coefficient for
```

```
!                  mmolN]        nitrification
!-------------------------------------------------------------------------!
&Param_parameters
! Switches :
            CalcPelagicFlag = .TRUE.
            CalcBenthicFlag = 0
       CalcConservationFlag = .FALSE.
          CalcTransportFlag = .FALSE.
        CalcPhytoPlankton(1) = .TRUE.
        CalcPhytoPlankton(2) = .TRUE.
        CalcPhytoPlankton(3) = .TRUE.
        CalcPhytoPlankton(4) = .TRUE.
          CalcPelBacteria(1) = .TRUE.
     CalcMicroZooPlankton(1) = .TRUE.
     CalcMicroZooPlankton(2) = .TRUE.
      CalcMesoZooPlankton(1) = .TRUE.
      CalcMesoZooPlankton(2) = .TRUE.
            CalcPelChemistry = .TRUE.
  AssignPelBenFluxesInBFMFlag = .FALSE.
  AssignAirPelFluxesInBFMFlag = .TRUE.
              ChlDynamicsFlag = 2
            check_fixed_quota = 0
! Parameters :
                    p_small = 1.0e-20
                       slp0 = 1013.25E0
                    p_pe_R1c = 0.60
                    p_pe_R1n = 0.72
                    p_pe_R1p = 0.832
                       p_qro = 0.5
                 p_qon_dentri = 1.25
                  p_qon_nitri = 2.0
filename_nml_conf = 'BFM_General.nml',
/


%!-------------------------------------------------------------------------!
%! NAMELIST bfm_init_nml
%!-------------------------------------------------------------------------!
%!Pelagic initialisation of standard variables
%!<variablename>0 = <realvalue>
%!-------------------------------------------------------------------------!
%&bfm_init_nml
%    O2o0 = 300.0,
%    N1p0 = 1.0,
%    N3n0 = 5.0,
%    N4n0 = 1.0,
%    N5s0 = 8.0,
%    N6r0 = 1.0,
%    O3c0 = 27060.00,
%    O3h0 = 2660.0,
%    O4n0 = 200.0,
%    P1c0 = 1.0,
%    P2c0 = 1.0,
%    P3c0 = 1.0,
%    P4c0 = 1.0,
%    Z3c0 = 1.0,
%    Z4c0 = 1.0,
%    Z5c0 = 1.0,
%    Z6c0 = 1.0,
%    B1c0 = 1.0,
%    R1c0 = 1.0,
%    R2c0 = 0.1,
%    R3c0 = 1.0,
%    R6c0 = 1.0,
%    filename_nml_conf = 'BFM_General.nml',
%/


%!-------------------------------------------------------------------------!
%!NAMELIST bfm_save_nml
%!-------------------------------------------------------------------------!
%! Stored variables
%!ave_save: average values over the output interval
%!var_save: instantaneous value at the output interval
%!-------------------------------------------------------------------------!
%&bfm_save_nml
%    var_save = ''
%    ave_save = 'ETW','O2o','DIC',
%           'EIR',
%           'xEPS',
%           'Chla',
%           'N1p','N3n','N4n','N5s',
%           'B1c',
%           'P1c','P2c','P3c','P4c',
%           'P1l','P2l','P3l','P4l',
%           'P1n','P2n','P3n','P4n',
%           'P1p','P2p','P3p','P4p',
%           'Z3c','Z4c','Z5c','Z6c',
%           'R1c','R2c','R6c',
%           'R1n','R6n',
%           'R1p','R6p',
%           'P1s','R6s',
%           'eiPPY(iiP1)','eiPPY(iiP2)','eiPPY(iiP3)','eiPPY(iiP4)',
%           'sunPPY(iiP1)','sunPPY(iiP2)','sunPPY(iiP3)','sunPPY(iiP4)',
%           'ruPPYc','resPBAc','resZOOc',
%           'ruPPYn','ruPPYp','ruPPYs','exPPYc',
%           'ruZOOc','remZOOn','remZOOp','remPBAn','remPBAp'
%
% filename_nml_conf = 'BFM_General.nml',
%/
%
%!-------------------------------------------------------------------------!
%!NAMELIST Settling_parameters
%!-------------------------------------------------------------------------!
%! BURIAL VELOCITIES into the sediment
%! NAME          [UNIT]/KIND              DESCRIPTION
%! p_burvel_R6    [m/d]                   Bottom Burial Velocity for detritus
%! p_burvel_R2    [m/d]                   Bottom Burial Velocity for dissolved
%! p_burvel_PI    [m/d]                   Bottom Burial Velocity for plankton
%!-------------------------------------------------------------------------!
%&Settling_parameters
%   p_burvel_R6 = 1.5,
%   p_burvel_R2 = 0.0,
```

```
%  p_burvel_PI = 0.0
% filename_nml_conf = 'Benthic_Environment.nml',
%/
%


!------------------------------------------------------------------------!
!NAMELIST CO2_parameters
!------------------------------------------------------------------------!
! CARBONATE SYSYEM SETTING
! NAME           [UNIT]/KIND           DESCRIPTION
! AtmCO20        [ppmv]                Initial atmospheric concentration of CO2
! calcAtmpCO2    logical               Compute the partial pressure of Atmospheric CO2
! pCO2Method     integer               pCO2 computation method: 1=MixRatio*slp0, 2=Magnus formula
! phstart        [pH]                  Initial pH value
! K1K2           integer               Switch for the acidity constants parameterization
!                                      1 : Roy et al. (1993); DOE (1994); pH on total scale
!                                      2 : Default. OCMIP STANDARD; pH on Sea Water Scale
!                                          Mehrbach et al (1973) refit by Dickson & Millero (1987)
!                                      3 : Mehrbach et al (1973) refit by Lueker et al. (2000)
!                                          pH on total scale
!                                      4 : Hansson (1973b) data as refitted by Dickson and
!                                          Millero (1987);  pH on Sea Water Scale
! MethodCalcCO2  numeric               Switch for the choice of [H+] numerical computation
!                                      1 : Approximate static solution
!                                      2 : Default. Standard OCMIP iteration
!                                      3 : Follows et al., Ocean Modelling 2006
! CalcBioAlkFlag logical               Compute biological processes corrections on total alkalinity
!               --------- Parameters for MethodCalcCO2=2 -----------
! M2XACC         real                  Accuracy of the iterative scheme for OCMIP (default 1.E-10)
! M2PHDELT       [pH]                  Delta of pH for the root search (realized pH+/-DELT)
!                                      in the OCMIP scheme (default 0.5)
! M2MAXIT        integer               Maximum number of iterations for OCMIP (default 100 )
!               --------- Parameters for calcium and calcite ---------
! Caconc0        [mol/m3]              Calcium ion concentration
!                                      ["Seawater : Its composition, properties and behaviour"
!                                      (2nd Edition), Open University Course Team, 1995]
!                                      Seawater concentration   = 412 mg / l
!                                                              -> atomic weight = 40.078 g / mol
!                                      therefore, concentration = 10.279 mmol / l = 10.279 mol / m3
! Canorm         logical               Normalize Calcium ion concentration by sea water salinity
!               --------- EXTERNAL DATA INPUT STRUCTURES -----------
! AtmCO2_N       structure             Read external data for atmospheric CO2 values
! AtmSLP_N       structure             Read external data for atmospheric sea level pressure
! AtmTDP_N       structure             Read external data for atmospheric dew-point temperature
! Example of general input structure for the data structure:
!          ! Read !   File                                 ! NetCDF ! Var    !
!          ! Input ! name                                  ! Logical ! name   !
!AtmCO2_N   =   0  , 'CMIP5_Historical_GHG_1765_2005.dat' , .FALSE.  , 'CO2'  ,
!          ! RefTime        ! Input      !   Time   !
!          ! yyyymmdd       ! Frequency  ! interp   !
!          '1764-07-01 00:00' ,  'yearly'  ,  .TRUE.
!
! Convention for Input reading : 0 = use constant value (default if structure is not initialized)
!                                2 = read timeseries file ( e.g. CO2 mixing ratios)
!                                4 = field from a coupled model (e.g. atmospheric SLP from OGCM)
! NOTE: The file "CMIP5_Historical_GHG_1765_2005.dat" is located in "$BFMDIR/tools" folder
!------------------------------------------------------------------------!
&CO2_parameters
   AtmCO20       = 370.0E0
   calcAtmpCO2   = .FALSE.
   pCO2Method    = 1
   AtmCO2_N  =   0  , 'CMIP5_Historical_GHG_1765_2005.dat' , .FALSE.  , 'CO2'  , '1764-07-01 00:00' , 'yearly'  , .TRUE.
   AtmSLP_N  =   0  , 'AtmSLP.nc' , .TRUE.  ,'AtmSLP' , '1764-07-01 00:00'  , 'dummy'  , .TRUE.
   AtmTDP_N  =   0  , 'AtmTDP.nc' , .TRUE.  ,'AtmTDP' , '1764-07-01 00:00'  , 'dummy'  , .TRUE.
   phstart       = 8.10E0
   K1K2          = 2
   MethodCalcCO2 = 2
  CalcBioAlkFlag = .FALSE.
         M2XACC = 1.0E-10
        M2PHDELT = 0.3
         M2MAXIT = 100
         Caconc0 = 10.279E0
         Canorm  = .TRUE.
filename_nml_conf = 'Carbonate_Dynamics.nml',
/


!------------------------------------------------------------------------!
!NAMELIST PelBac_parameters
!------------------------------------------------------------------------!
!  PELAGIC BACTERIA
!
! NAME           [UNIT]/KIND           DESCRIPTION
! p_version      integer               Switch for bacteria parameterization
!                                      1 : Baretta-Bekker et al. 1995;
!                                          Vichi et al., 2007
!                                      2 : Vichi et al., 2004
!                                      3 : Polimene et al., 2006
! p_q10          [-]                   Q10-value (temperature dependency)
! p_chdo         [mmol/m3]             Half-saturation constant for O2 limitation
! p_sd           [1/d]                 Specific mortality rate
! p_sd2          [1/d]                 Density dependent specific mortality rate
! p_suhR1        [1/d]                 Specific potential uptake for nutrient-rich DOM
! p_sulR1        [1/d]                 Specific potential uptake for nutrient-poor DOM
! p_suR2         [1/d]                 Specific potential uptake for semi-labile DOC
! p_suR3         [1/d]                 Specific potential uptake for semi-refractory DOC
! p_suR6         [1/d]                 Specific potential uptake for POM (1/d)
! p_sum          [1/d]                 Potential specific growth rate
! p_pu_ra        [-]                   Activity respiration fraction
! p_pu_ra_o      [-]                   Additional respiration fraction at low O2 conc
! p_srs          [1/d]                 Specific rest respiration
! p_qncPBA       [mmolN/mgC]           Optimal N/C ratio
! p_qpcPBA       [mmolP/mgC]           Optimal P/C ratio
! p_qlnc         [mmolN/mgC]           Minimal N/C ratio
! p_qlpc         [mmolP/mgC]           Minimal P/C ratio
! p_qun          [mmolN/mgC/day]       Membrane affinity for N
! p_qup          [mmolP/mgC/day]       Membrane affinity for N
! p_chn          [mmolN/m3]            Half saturation ammonium conc. for uptake
! p_chp          [mmolP/m3]            Half saturation phosphate conc. for uptake
! p_ruen         [1/d]                 Relaxation timescale for N uptake/remin.
! p_ruep         [1/d]                 Relaxation timescale for P uptake/remin.
```

```
!   p_rec       [1/d]          Relaxation timescale for semi-labile excretion
!   p_pu_ea_R3  [-]            Excretion of semi-refractory DOC
!-------------------------------------------------------------------------!
&PelBacteria_parameters
!               B1
       p_version = 2
           p_q10 = 2.95
          p_chdo = 30.0
            p_sd = 0.0
           p_sd2 = 0.0
         p_suhR1 = 0.5
         p_sulR1 = 0.0
          p_suR2 = 0.25
          p_suR3 = 0.0
          p_suR6 = 0.1
           p_sum = 8.38
         p_pu_ra = 0.6
       p_pu_ra_o = 0.2
           p_srs = 0.01
        p_qncPBA = 0.017
        p_qpcPBA = 0.0019
          p_qlnc = 0.0085
          p_qlpc = 0.00095
           p_qun = 0.05
           p_qup = 0.005
           p_chn = 0.05
           p_chp = 1.00
           p_rec = 1.0
          p_ruen = 1.0
          p_ruep = 1.0
       p_pu_ea_R3 = 0.0
filename_nml_conf = 'Pelagic_Ecology.nml',
/


!-------------------------------------------------------------------------!
!NAMELIST Phyto_parameters, Phyto_parameters_iron
!-------------------------------------------------------------------------!
!   PELAGIC PHYTOPLANKTON
!   NAME        [UNIT]/KIND         DESCRIPTION
!       :       --------- Physiological parameters ----------------
!   p_q10       [-]            Characteristic Q10 coefficient
!   p_qtemp     [-]            Cut-off threshold for temperature factor
!   p_sum       [1/d]          Maximal productivity at 10 degrees C
!   p_srs       [1/d]          Respiration rate at 10 degrees C
!   p_sdmo      [1/d]          Max.specific nutrient-stress lysis rate
!   p_thdo      [-]            Half saturation constant for nutrient stress lysis
!   p_seo       [1/d]          Extra lysis rate (biomass density-dependent)
!   p_sheo      [mgC/3]        Half saturation constant for extra lysis
!   p_pu_ea     [-]            Excreted fraction of primary production
!   p_pu_ra     [-]            Activity respiration fraction
!   p_switchDOC [1-3]          Switch for the type of DOC excretion
!                              This choice must be consistent with bacteria
!                              1. All DOC is released as R1c (Vichi et al., 2007)
!                              2. Activity DOC is released as R2c (Vichi et al., 2004)
!                                 (there is no nutrient-stress excretion)
!                              3. All DOC is released as R2c (Polimene et al., 2006)
!
!               --------- Nutrient parameters in phytoplankton ----------------
!   p_netgrowth [T or F]       Logical switch for nutrient-limited growth
!                              .T. nutrient-balanced growth (Vichi et al.2004)
!                              .F. nutrient-stress carbon excretion
!                                 (Baretta-Bekker et al.1995 and Vichi et al.2007)
!   p_limnut    [1-3]          Switch for N-P co-limitation
!                              0. Geometric mean
!                              1. Threshold (Liebig-like)
!                              2. Combined
!                    ---- N limitation control ----
!   p_qun       [m3/mgC/d]     Membrane affinity for N
!   p_lN4       [mmolN/m3]     Half saturation constant for NH4 uptake preference over NO3
!   p_qnlc      [mmolN/mgC]    Minimum quotum Si:C
!   p_qncPPY    [mmolN/mgC]    Reference quotum Si:C
!   p_xqn       [-]            Multiplication factor for luxury storage
!                    ---- P limitation control ----
!   p_qup       [m3/mgC/d]     Membrane affinity for P
!   p_qplc      [mmolP/mgC]    Minimum quotum Si:C
!   p_qpcPPY    [mmolP/mgC]    Reference quotum Si:C
!   p_xqp       [-]            Multiplication factor for luxury storage
!                    ---- Si limitation control ----
!   p_switchSi  [1-2]          Switch for Silica limitation
!                              1. Si limitation is controlled by external Si conc.
!                              2. Si limitation is controlled by internal quota
!   p_chPs      [mmolSi/m3]    Half saturation conc. for dissolved Si limitation
!   p_Contois   [>=0]          If >0, use Contois formulation
!   p_qus       [m3/mgC/d]     Membrane affinity for Si
!   p_qslc      [mmolSi/mgC]   Minimum quotum Si:C
!   p_qscPPY    [mmolSi/mgC]   Reference quotum Si:C
!                              Brzezinski (1985) 0.13 mol/mol
!                    ---- nutrient stressed sinking ----
!   p_esNI      [-]            Nutrient stress threshold for sinking
!   p_res       [m/d]          Maximum Sinking vel city (m/d)
!                 --------- Chlorophyll parameters -----------
!   p_switchChl [1-4]          Switch for Chla-a synthesis
!   p_sdchl     [1/d]          Specific turnover rate for Chla
!   p_alpha_chl [mgC s m2/     Initial slope of the P-E curve
!                mgChl/uE]
!   p_qlcPPY    [mgChla/mgC]   Reference quotum Chla:C
!   p_epsChla   [m2/mgChla]    Chla-specific extinction coefficient
!   p_tochl_relt [1/d]         Relaxation rate towards maximum Chla:C
!   p_EpEk_or   [-]            Optimal value of E_PAR/E_K
!                 --------- Iron parameters -----------
!   p_quf       [m3/mgC/d]     Membrane affinity for Fe
!   p_qflc      [umolFe/mgC]   Minimum quotum Fe:C derived from 3 umol Fe/mol C
!                              Sunda & Huntsman (1997), Nature, 390, p 389-392
!   p_qfcPPY    [umolFe/mgC]   Reference quotum Fe:C
!   p_xqf       [-]            Multiplication factor for luxury storage
!                 --------- Light parameters ERSEM-II -----------
!   p_iswLtyp   [0-6]          Shape of the productivity function
!   p_chELiPPY  [W/m2]         Maximum Iopt
!   p_clELiPPY  [W/m2]         Minimum Iopt
!   p_ruELiPPY  [1/d]          Maximum daily shift in Iopt (1/d)
!   p_addepth   [m]            Adaptation depth. Meaningless with high-res models
```

```
!             --------- Sinking parameters -----------
! p_rPIm     [m/d]          Phytoplankton background sinking rate
!-----------------------------------------------------------------------!
&Phyto_parameters
!               P1      P2      P3      P4
        p_q10 = 2.0,    2.0,    2.0,    2.0
       p_temp = 0.0,    0.0,    0.75,   0.0
        p_sum = 2.5,    3.0,    3.5,    1.5
        p_srs = 0.1,    0.05,   0.1,    0.1
       p_sdmo = 0.0,    0.0,    0.0,    0.0
       p_thdo = 0.0,    0.0,    0.0,    0.0
        p_seo = 0.0,    0.0,    0.0,    0.0
       p_sheo = 0.0,    0.0,    0.0,    100.0
      p_pu_ea = 0.05,   0.1,    0.1,    0.15
      p_pu_ra = 0.1,    0.1,    0.2,    0.1
   p_switchDOC = 2,     2,      2,      2
   p_netgrowth = .TRUE.,.TRUE.,.TRUE.,.TRUE.
      p_limnut = 1,     1,      1,      1
        p_qun = 0.025,  0.025,  0.25,   0.025
        p_lN4 = 1.0,    0.5,    0.1,    1.0
       p_qnlc = 0.00687, 0.00687, 0.00687, 0.00687
     p_qncPPY = 1.26e-2,1.26e-2,1.26e-2,1.26e-2
        p_xqn = 2.0,    2.0,    2.0,    2.0
        p_qup = 0.0025, 0.0025, 0.0025, 0.0025
       p_qplc = 0.0004288,0.0004288,0.0004288,0.0004288
     p_qpcPPY = 7.86e-4,7.86e-4,7.86e-4,7.86e-4
        p_xqp = 2.0,    2.0,    2.0,    2.0
   p_switchSi = 2,      0,      0,      0
        p_chPs = 0.3,   0.0,    0.0,    0.0
    p_Contois = 0.0,    0.0,    0.0,    0.0
        p_qus = 0.0025,    0.0,    0.0,    0.0
       p_qslc = 0.007,     0.0,    0.0,    0.0
     p_qscPPY = 0.01,   0.0,    0.0,    0.0
       p_esNI = 0.7,    0.75,   0.75,   0.75
        p_res = 5.0,    0.0,    0.0,    2.5
   p_switchChl = 2,     2,      2,      2
       p_sdchl = 0.2,   0.2,    0.2,    0.2
   p_alpha_chl = 2.50e-5, 1.70e-5, 2.75e-5, 0.68e-5
      p_qlcPPY = 0.02,  0.02,   0.02,   0.02
     p_epsChla = 0.03,  0.03,   0.03,   0.03
     p_EpEk_or = 0.0,   0.0,    0.0,    0.0
   p_tochl_relt = 0.0,  0.0,    0.0,    0.0
     p_iswLtyp = 5,     5,      5,      5
     p_addepth = 50.0,  50.0,   50.0,   50.0
    p_chELiPPY = 100.0, 100.0,  100.0,  100.0
    p_clELiPPY = 8.0,   10.0,   6.0,    12.0
    p_ruELiPPY = 0.2,   0.25,   0.3,    0.15
        p_rPIm = 0.0,   0.0,    0.0,    0.0
filename_nml_conf = 'Pelagic_Ecology.nml',
/


&Phyto_parameters_iron
filename_nml_conf = 'Pelagic_Ecology.nml',
/


!-----------------------------------------------------------------------!
!NAMELIST PAR_parameters
!-----------------------------------------------------------------------!
! LightPeriodFlag   numeric Choose the light averaging period
!                           1 = Instantanous irradiance
!                           2 = Daily average
!                           3 = Daylight average with explicit
!                               photoperiod
! LightLocationFlag numeric Choose the parameterization of light
!                           location in the discrete grid
!                           1 = Light at the top of the cell
!                           2 = Light in the middle of the cell
!                           3 = Average Light in the cell
! ChlAttenFlag      numeric Choose the PAR attenuation due to Chl
!                           1 = broadband linear attenuation
!                           2 = 3-band tabulated attenuation coefficients
!                               (Morel, 1988; Lengaigne et al, 2007)
! p_PAR       [-]           Fraction of Photosynthetically Available Radiation
! p_eps0      [1/m]         Background extinction coefficient
! p_epsIR     [1/m]         Infrared extinction coefficient
!                           (to use with ChlAttenFlag=2)
! p_epsESS    [m2/g]        Specific attenuation coefficient of
!                           suspended sediments
! p_epsR6     [m2/mgC]      Specific attenuation coefficient of particulate
!                           detritus
!-----------------------------------------------------------------------!
&PAR_parameters
  LightPeriodFlag   = 1
  LightLocationFlag = 2
  ChlAttenFlag      = 1
  p_PAR       = 0.40
  p_eps0      = 0.0435
  p_epsIR     = 2.857
  p_epsESS    = 0.04d-3
  p_epsR6     = 0.1d-3
filename_nml_conf = 'Pelagic_Environment.nml',
/


!-----------------------------------------------------------------------!
!NAMELIST MicroZoo_parameters
!-----------------------------------------------------------------------!
!  MICRO-ZOOPLANKTON
!
! NAME        [UNIT]/KIND        DESCRIPTION
! p_q10       [-]           Q10 value for physiological rates
! p_srs       [1/d]         Respiration rate at 10 degrees Celsius
! p_sum       [1/d]         Potential growth rate
! p_sdo       [1/d]         Mortality rate due to oxygen limitation
! p_sd        [1/d]         Temperature independent mortality rate
! p_pu        [-]           Assimilation efficiency
! p_pu_ea     [-]           Fraction of activity excretion
! p_chro      [mmolO2/m3]   Half-saturation oxygen concentration
! p_chuc      [mgC/m3]      Half-saturation Food concentration for Type II
! p_minfood   [mgC/m3]      Half-saturation food concentration for
!                           preference factor
! p_qncMIZ    [mmolN/mgC]   Maximum quotum P:C
```

```
! p_qpcMIZ      [mmolN/mgC]     Maximum quotum N:C
! p_paPBA(z,b) [-]              Availability of pelagic Bacteria group b
!                               to Zooplankton group z
! p_paPPY(z,p) [-]              Availability of PhytoPlankton group p
!                               to Zooplankton group z
! p_paMIZ(z,m) [-]              Availability of MicroZooplankton group m
!                               to Zooplankton group z
!-------------------------------------------------------------------!
&MicroZoo_parameters
!            Z5       Z6
     p_q10 = 2.0,     2.0
     p_srs = 0.02,    0.02
     p_sum = 2.0,     5.0
     p_sdo = 0.05,    0.05
      p_sd = 0.0,     0.0
      p_pu = 0.5,     0.3
    p_pu_ea = 0.5,    0.5
    p_chro = 8,       8
    p_chuc = 30.0,    100.0
  p_minfood = 50.0,   50.0
   p_qpcMIZ = 1.85d-3,1.85d-3
   p_qncMIZ = 1.67d-2,1.67d-2
! Food matrix parameters: take care of the notation
!            Z5       Z6
   p_paPBA = 0.1,     1.0
!            P1       P2       P3       P4
!     Z5
p_paPPY(1,:) = 0.7,   1.0,     0.1,     0.1
!     Z6
p_paPPY(2,:) = 0.0,   0.2,     1.0,     0.0
!            Z5       Z6
!     Z5
p_paMIZ(1,:) = 1.0,   1.0
!     Z6
p_paMIZ(2,:) = 0.0,   0.2
filename_nml_conf = 'Pelagic_Ecology.nml',
/


!-------------------------------------------------------------------!
!NAMELIST MesoZoo_parameters
!-------------------------------------------------------------------!
!  MESO-ZOOPLANKTON
! NAME        [UNIT]/KIND         DESCRIPTION
! p_q10       [-]             Q10 value for physiological rates
! p_srs       [1/d]           Respiration rate at 10 degrees C
! p_sum       [1/d]           Maximal productivity at 10 degrees C
! p_sd        [1/d]           Background natural mortality
! p_vum       [m3/mgC/d]      Specific search volume
! p_puI       [-]             Assimilation efficiency
! p_peI       [-]             Fraction of Faeces production
! p_sdo       [m3/mgC/d]      Specific density-dependent mortality
! p_sds       [-]             Exponent of density-dependent mortality
! p_qpcMEZ    [mmolP/mgC]     Maximum quotum P:C
! p_qncMEZ    [mmolN/mgC]     Maximum quotum N:C
! p_clO2o     [mmolO2/m3]     Half-saturation oxygen concentration
! p_paPPY(z,p) [-]            Availability of PhytoPlankton group p
!                             to Zooplankton group z
! p_paMIZ(z,m) [-]            Availability of MicroZooplankton group m
!                             to Zooplankton group z
! p_paMEZ(z,m) [-]            Availability of MesoZooplankton group m
!                             to Zooplankton group z
!-------------------------------------------------------------------!
&MesoZoo_parameters
!            Z3       Z4
     p_q10 = 2.0,     2.0
     p_srs = 0.01,    0.02
     p_sum = 2.0,     2.0
     p_vum = 0.008,   0.02
     p_puI = 0.6,     0.6
     p_peI = 0.3,     0.35
     p_sdo = 0.01,    0.01
      p_sd = 0.02,    0.02
     p_sds = 2.0,     2.0
   p_qpcMEZ = 1.67d-3,1.67d-3
   p_qncMEZ = 0.015,  0.015
   p_clO2o = 30.0,    30.0
! Food matrix parameters: take care of the notation
!            P1       P2       P3       P4
!     Z3
p_paPPY(1,:) = 0.0,   0.0,     0.0,     1.0
!     Z4
p_paPPY(2,:) = 1.0,   0.75,    0.0,     1.0
!            Z5       Z6
!     Z3
p_paMIZ(1,:) = 0.0,   0.0
!     Z4
p_paMIZ(2,:)= 1.0,    0.0,
!            Z3       Z4
!     Z3
p_paMEZ(1,:)= 1.0,    1.0
!     Z4
p_paMEZ(2,:)= 0.0,    1.0
filename_nml_conf = 'Pelagic_Ecology.nml',
/


!-------------------------------------------------------------------!
!NAMELIST PelChem_parameters, PelChem_parameters_iron
!-------------------------------------------------------------------!
!  Pelagic Chemistry parameters
! NAME        [UNIT]/KIND     DESCRIPTION
! p_q10N4N3   [-]             Q10 factor for nitrification/denit
! p_sN4N3     [1/d]           Specific nitrification rate at 10 degC
! p_clO2o     [mmolO2/m3]     Half-saturation O2 concentration for
!                             nitrification and reoxidation
! p_rOS       [1/d]           Specific reoxidation rate of reduction
!                             equivalents
! p_sN3O4n    [1/d]           Specific denitrification rate
! p_clN6r     [mmolHS/m3]     Half-saturation concentration of
!                             reduction equivalents for denitrification
! p_rPAo      [mmolO2/m3/d]   Reference anoxic mineralization rate
! p_q10R6N5   [-]             Q10 factor for biogenic silica
```

```
! p_sR6N5     [1/d]          Specific remineralization rate of
!                            biogenic silica
!         --------- Iron parameters -----------
! p_q10R6N7   [-]            Q10 temperature dependence
! p_sR6N7     [1/d]          Specific remineralization rate of particulate
! p_sR1N7     [1/d]          Specific remineralization rate of dissolved
! p_scavN7f   [1/d]          Specific scavenging rate
! p_N7fsol    [umolFe/m3]    Solubility concentration
!------------------------------------------------------------------------!
&PelChem_parameters
  p_q10N4N3 = 2.367
    p_sN4N3 = 0.01
    p_clO2o = 10.0
      p_rOS = 0.05
   p_sN3O4n = 0.35
    p_clN6r = 1.0
     p_rPAo = 1.0
  p_q10R6N5 = 1.49
    p_sR6N5 = 0.1
filename_nml_conf = 'Pelagic_Environment.nml',
/


&PelChem_parameters_iron
filename_nml_conf = 'Pelagic_Environment.nml',
/


!------------------------------------------------------------------------!
!NAMELIST PelGlobal_parameters
!------------------------------------------------------------------------!
! Sinking rates of Pelagic Variables
!  : for mem_PelGlobal filled by InitPelGlobal
! NAME           UNIT      DESCRIPTION
! p_rR6m         [m/d]     detritus sinking rate
! KSINK_rPPY     [m]       prescribe sinking rate for phytoplankton below this
!                          depth threshold to p_rR6m value. Use 0.0 to disable.
! AggregateSink  logic     use aggregation = true to enhance the sink rate
!                          and bypass the prescribed sinking
! depth_factor   [m]       depth factor for aggregation method
!------------------------------------------------------------------------!
&PelGlobal_parameters
  p_rR6m        = 5.0
  KSINK_rPPY    = 150.0
  AggregateSink = .FALSE.
  depth_factor  = 2000.0
filename_nml_conf = 'Pelagic_Environment.nml',
/


!------------------------------------------------------------------------!
!NAMELIST standalone_nml
!------------------------------------------------------------------------!
!NAME KIND DESCRIPTION
!nboxes  integer Number of water volumes (boxes)
!indepth  real  Depth of each box (m)
!latitude  real  Latitude of each box
!longitude  real  Longitude of each box
!maxdelt  real  Maximum timestep duration (s)
!mindelt  real  Minimum timestep duration (s)
!method  integer Integration method
! 1. Euler forward
! 2. Runge-Kutta 2nd order
! 3. Leap-frog
!----------------------------------------------------------------------
&standalone_nml
   nboxes     = 1,
   indepth    = 5.0,
   latitude   = 45.0,
   longitude  = 13.5,
   maxdelt    = 8640.0,
   mindelt    = 1.0,
   method     = 2,
filename_nml_conf = 'Standalone.nml',
/

!------------------------------------------------------------------------!
!NAMELIST time_nml
!------------------------------------------------------------------------!
!Specify time related formats and variables here.
!timefmt integer implicitly uses timestep=maxdelt
!                1- MaxN only - fake start time used.
!                2- start and stop - MaxN calculated.
!                3- start and MaxN - stop calculated.
!                4- simdays - fake start time used
!    and MaxN calculated.
!MaxN integer do loop from n=1,MaxN
!start string Initial time: YYYY/MM/DD HH:MM:SS
!stop string Final   time: YYYY/MM/DD HH:MM:SS
!------------------------------------------------------------------------!
 &time_nml
  timefmt=      2,
  MaxN=         144,
  simdays=      5760,
  start=        "2000-01-01 00:00:00",
  stop=         "2010-01-01 00:00:00",
filename_nml_conf = 'Standalone.nml',
/


!------------------------------------------------------------------------!
!NAMELIST forcings_nml
!------------------------------------------------------------------------!
!forcing_method integer Choice of the external forcing functions
! 1 = analytical forcings
! 2 = from file
! 3 = interactive fluxes (not yet implemented)
!
!Method 1: Analytical forcing functions
!lw real Sinusoidal light intensity (winter) W m^-2
!ls real Sinusoidal light intensity (summer) W m^-2
!sw real Sinusoidal salinity (winter)
!ss real Sinusoidal salinity (summer)
!tw real Sinusoidal temperature (winter) degC
!ts real Sinusoidal temperature (summer) degC
```

```
!tde real Sinusoidal temperature daily excursion degC
!ww real Sinusoidal wind (winter) m/s
!ws real Sinusoidal wind (summer) m/s
!CO2inc         real    Linear increase in CO2 air partial pressure [% per year]
!
!Method 2: data file
!forcing_file char Filename for external forcings
!
!use_external_data logical Read external data (user defined)
!data_file    char    Filename for external data
!
!----------------------------------------------------------------------!
&forcings_nml
   forcing_method   = 1,
   ltype            = 1,
   lw               = 20.0,
   ls               = 300.0,
   sw               = 37.0,
   ss               = 34.0,
   tw               = 8.0,
   ts               = 28.0,
   tde              = 1.0,
   ww               = 20.0,
   ws               = 10.0,
   forcing_file     = '',
   use_external_data = .false.,
   data_file        = '',
filename_nml_conf = 'Standalone.nml',
/


!-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-
! MODEL  BFM - Biogeochemical Flux Model
!-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-
```

4 Results: Sensitivity Analysis

In addition to the DCM depth, the skill in reproducing DCM thickness and Chl concentration in the DCM layer were also analysed. DCM thickness is operationally defined through a Gaussian fit as $\pm\sigma/2$ from the maximum. The Chl concentration at DCM is in turn averaged over the DCM thickness. For REF and CL1 simulations, skills are compared also at the surface layer (0 - 25 m). To avoid corrections due to non-photochemical quenching, profiles acquired only during stratified periods were considered. In order to further evaluate the dependence of model results on PAR forcing, two numerical experiments were carried out. In the first experiment, BGC-Argo floats were divided in couples composed by one trajectory located in the western basin and the other one in the eastern basin, by random selection. For each couple the initial conditions for nutrients were interchanged, which allows to estimate their impact on DCM depth. Results Fig. S1 evidence that the inverted initialization of nutrients does not significantly alter the outcome in terms of DCM depth, resulting in a slope reduction from 0.81 to 0.62, and maintaining similar correlation and bias. Thus it appears that the role of nutrients is secondary compared to the impact of light on DCM depth regulation on such time scales.

Performing the same operation by switching light data instead of nutrients proves to be technically more complex, thus an alternative approach was applied, which consists of a sensitivity analysis similar to the one described in Huisman et al.(2004). Such technique allows to further understand the driving mechanisms of DCM depth variability. For this purpose, two BGC-Argo floats (lovbio018c and lovbio067c for east and west respectively) and phosphate and PAR parameters were selected, constructing an array of 21x21=441 simulations (per float) for bivariate perturbations.

A perturbation of 50% of the of initial phosphate (PO_4) condition has only a minor effect on DCM depth position (Fig. S2) while changes in light conditions show a larger effect (approximately 10 m difference).

The same sensitivity analysis is used to evaluate the model performance in reproducing the DCM width and the Chl concentrations at the DCM (plots for both lovbio018c and lovbio067c are reported at the end of the section, Fig. S6, Fig. S7, Fig. S8). Results indicate that the DCM width has a variability of 6 m in the perturbation range ($\pm$50%), as well as that the DCM magnitude is controlled by nutrient availability rather than light. Comparing measured Chl concentrations and model results shows that the skill in reproducing the DCM thickness is lower compared to the DCM depth (Fig. S3, r=0.55, slope=0.6).

The DCM thickness varies between 20 and 40 m for the model, whereas a higher variability from 5 m to 40 m is measured by BGC-Argo (Fig. S3). Average surface Chl in 0-25 m (Fig. 10 reported in the main text of the article) layer shows similar skill (r=0.68, slope=0.63) as in the case of DCM thickness.

The skill of the 1-D model in reproducing the biomass at DCM is lower than for the other indicators: measured Chl concentration fluctuates in the DCM and the possible underlying mechanism (e.g. presence of Rossby waves or Kelvin waves) goes beyond the scope of the present paper. The median Chl in the DCM layer ($\pm\sigma/2$) for each BGC-Argo float (Fig. S4). Following the procedure of the sensitivity analysis shown before, we evaluated the effects of perturbing nutrients for the BGC-Argo floats deployed in the West Mediterranean by increasing them by a factor 2 (orange dots, Fig. S4). The skill in reproducing the DCM depth is almost the same between REF and REF with higher nutrients, Fig.S5, however changes in initial nutrient concentrations have a significant impact on the Chl concentration at DCM. Therefore, it should be possible to finely tune the initial conditions to maximize both skills in terms of DCM value and DCM depth. However, consider-
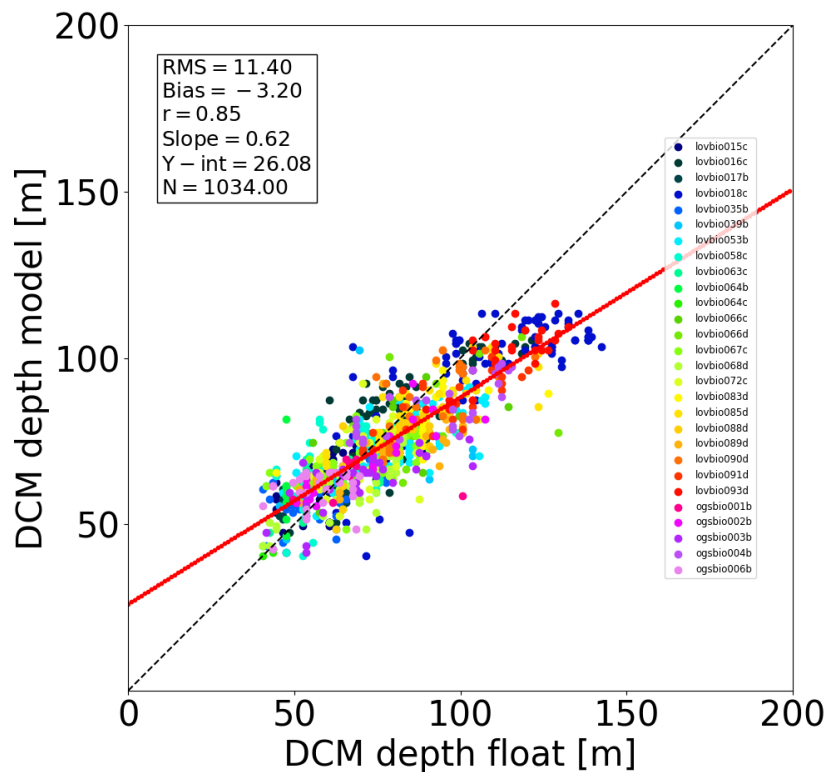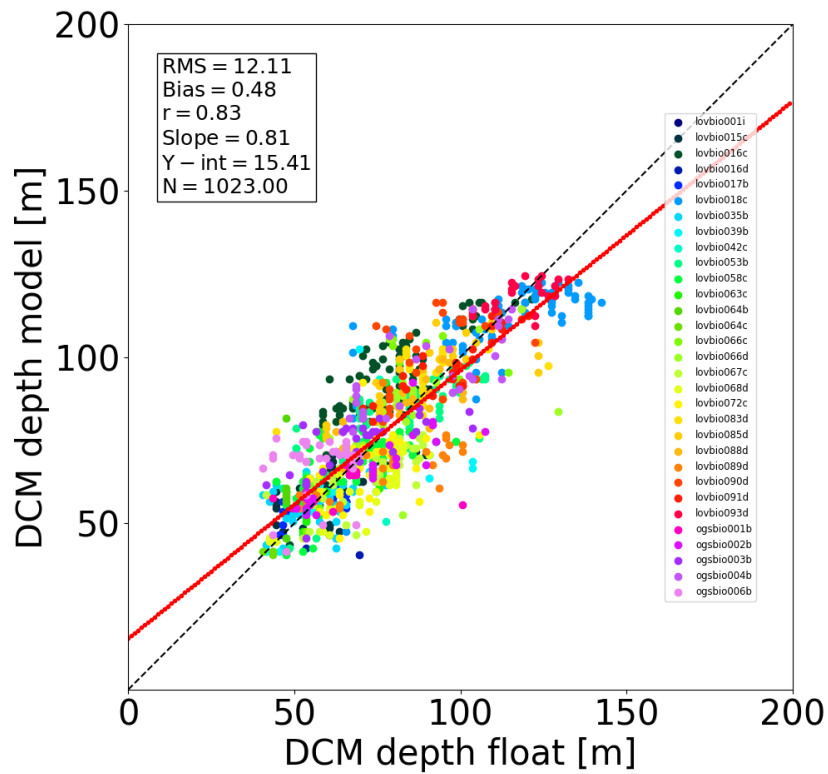
Figure S1: Scatter plots of DCM depth derived for the REF simulation (TOP) and with the "East-West" switching technique described in the text (BOTTOM).

ing the fact that the measurements of Chl concentrations derived from fluorescence present some uncertainties Roesler et al (2017), Barbieux et al. (2018), Organelli et al. (2017), we chose to keep the initialization based on reanalysis.
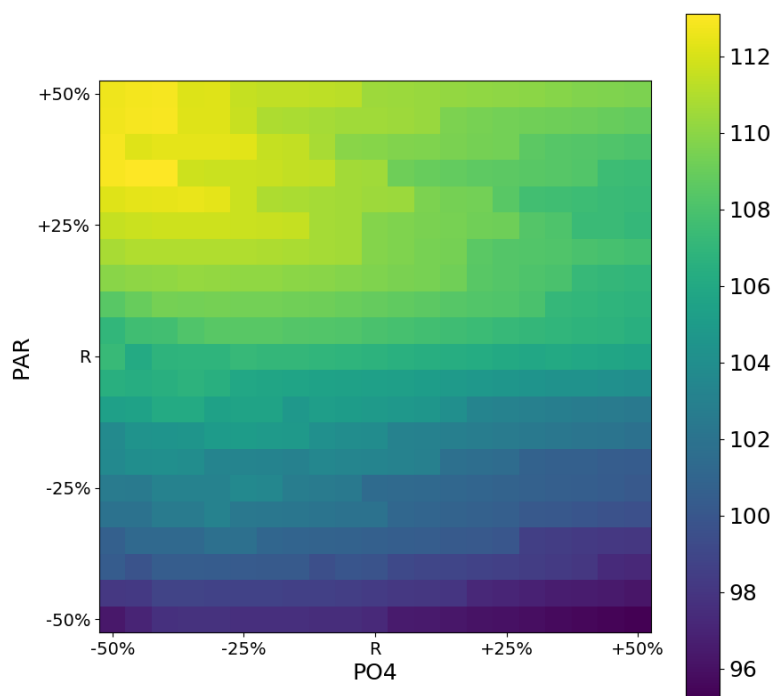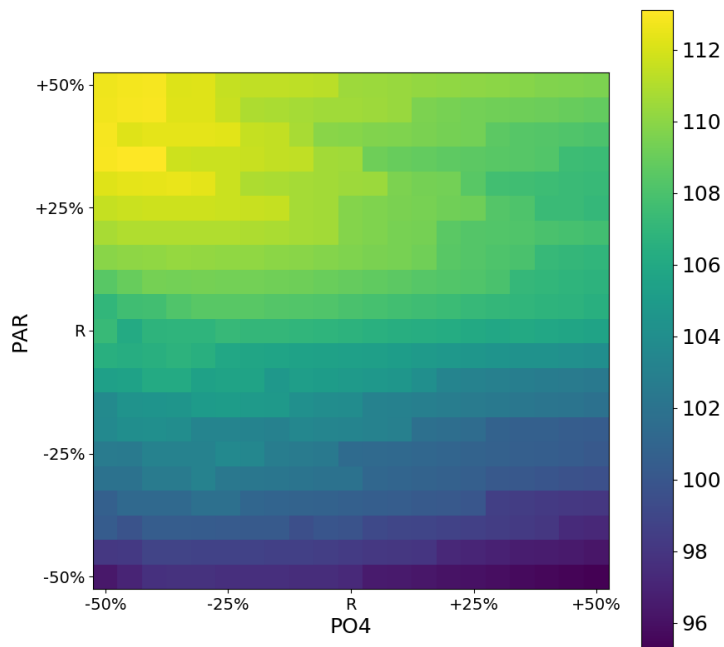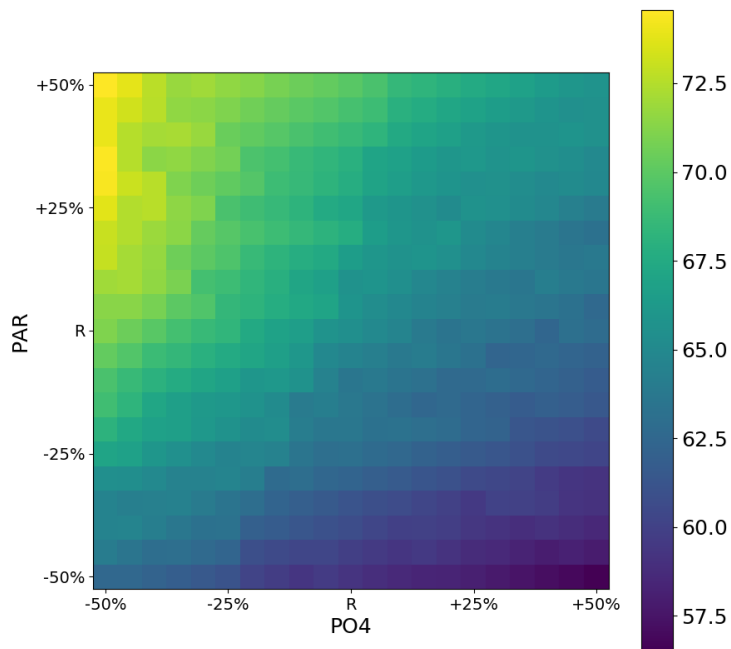
Figure S2: Sensitivity analysis of DCM depth perturbing light and initial conditions of PO4 (both by an uniform factor reported on axis in percentage) along the water column. 'R' marks the reference values. The BGC-Argo float here reported is the lovbio018c. Each pixel is a full simulation of a total of 21x21 simulations. The DCM depth is averaged over the simulation period.
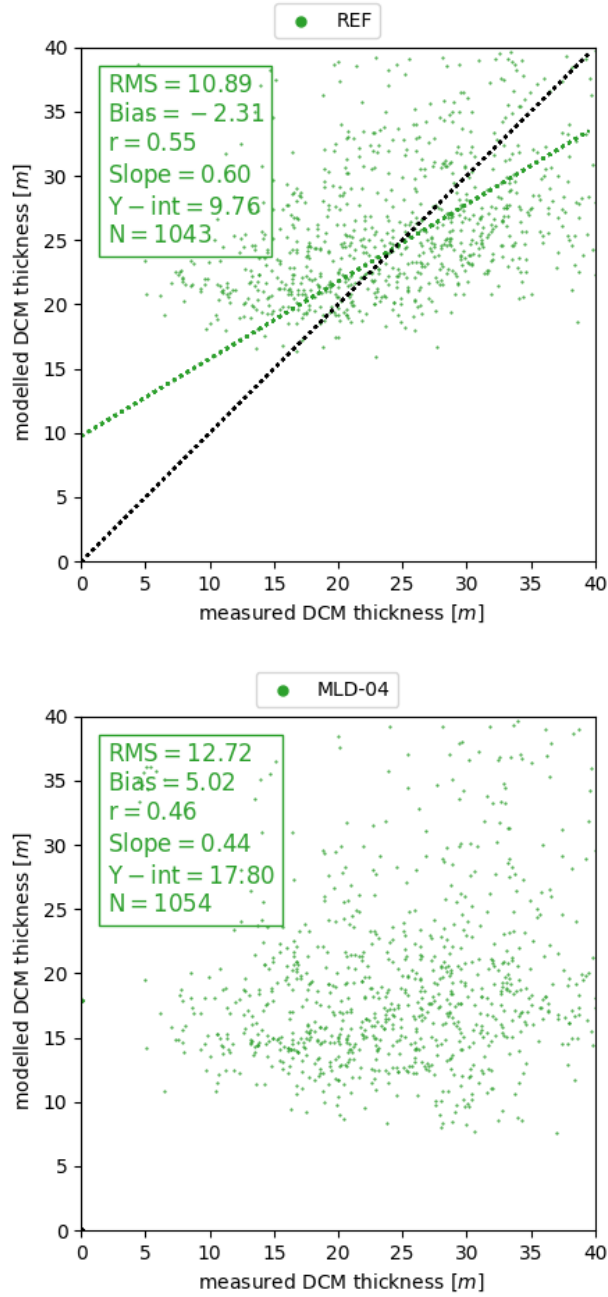
Figure S3: Scatter plot of DCM thickness. Top panel reports REF simulation ($D_v^{background} = 10^{-4} m^2 s^{-1}$), bottom panel shows MLD04 simulation ($D_v^{background} = 10^{-6} m^2 s^{-1}$). The thickness is defined as $\pm \sigma/2$ centered on the maximum computed on the vertical profiles by means of a Gaussian fit.
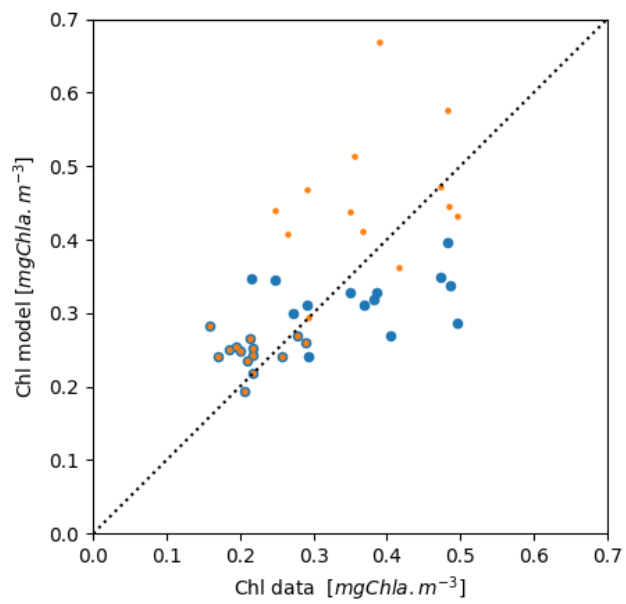
Figure S4: Scatter plot of DCM Chl concentration as defined in the text: median concentration of the REF (blue dots) and from the simulation increasing PO4 (orange dots).
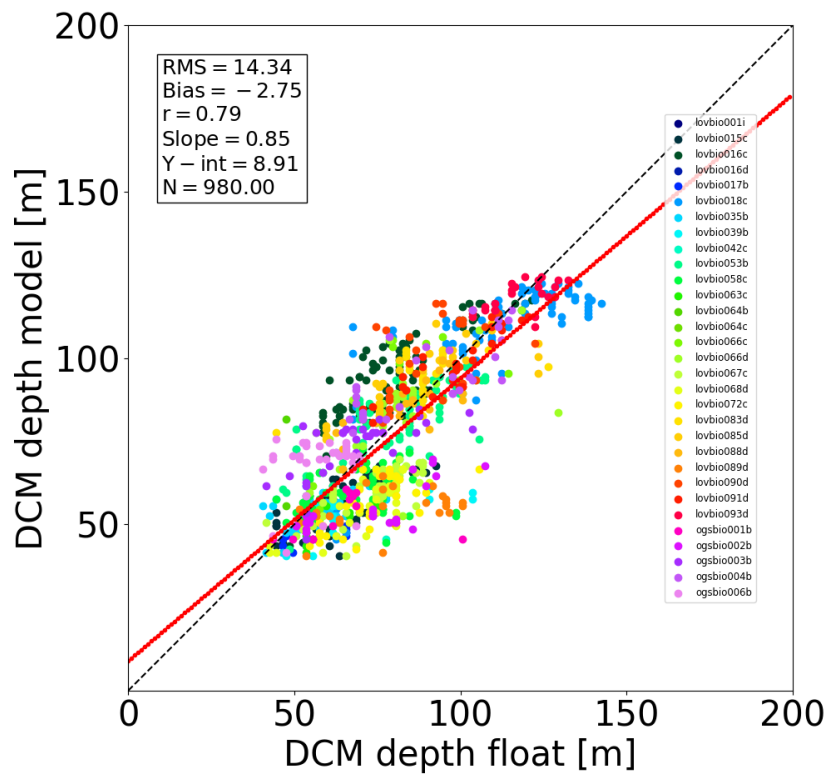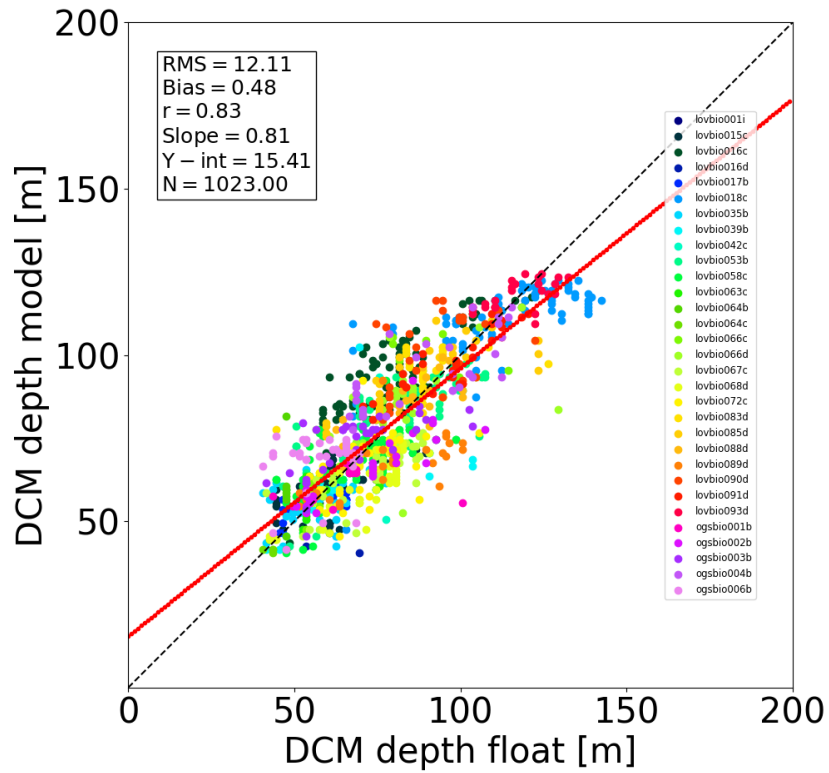
Figure S5: Scatter plots of DCM depth derived for the REF simulation (TOP) and with the double nutrient initial conditions for the West Basin (BOTTOM).

The following figures show the sensitivity of three selected indicators when light and phosphate are independently perturbed, from -50% to +50%. This generates an array of 21X21 simulations of which the central one is the reference. Each pixel of the following shaded plots is a different simulation. Two BGC Argo floats are considered the lovbio067c and lovbio018c respectively top and bottom panel of each figure. The indicators considered are DCM depth (Fig.S6), DCM width (Fig.S7) and chlorophyll concentration at DCM (Fig.S8).
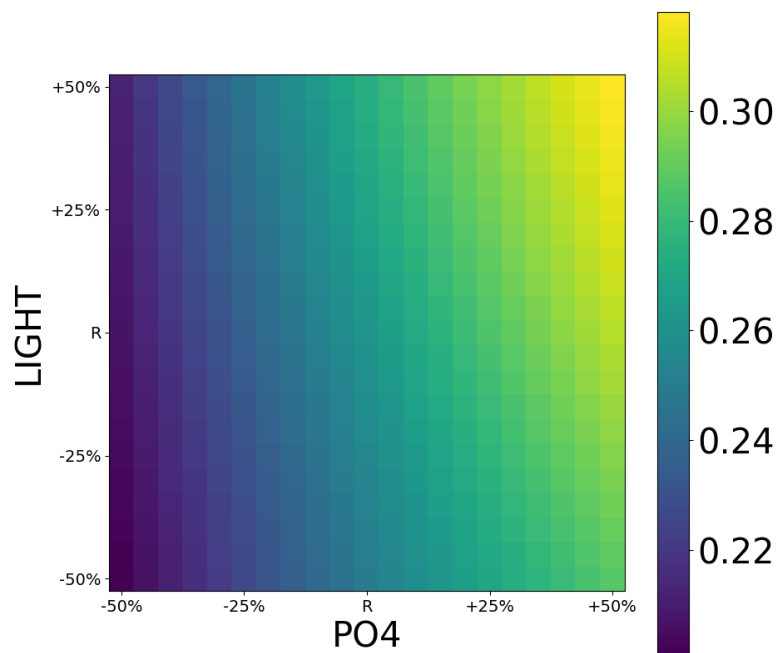
Figure S6: Sensitivity analysis of DCM depth perturbing LIGHT and perturbing initial conditions of PO4 [both by an uniform factor reported on axis in percentage] along the water column. 'R' marks the reference values. The BGC-Argo floats here reported are the lovbio067c (top) and the lovbio018c (bottom). Each pixel is a full simulation, for a total of 21x21 simulations. The DCM depth is averaged over the simulation period.
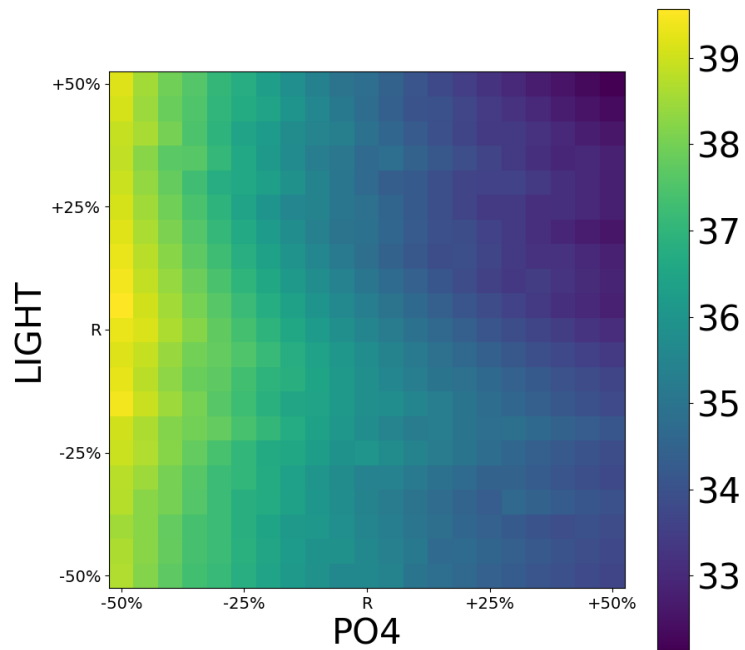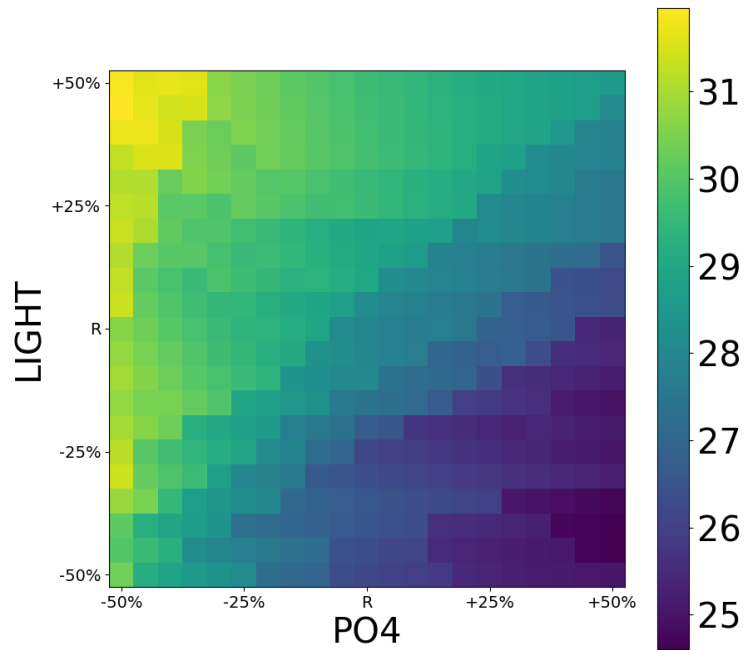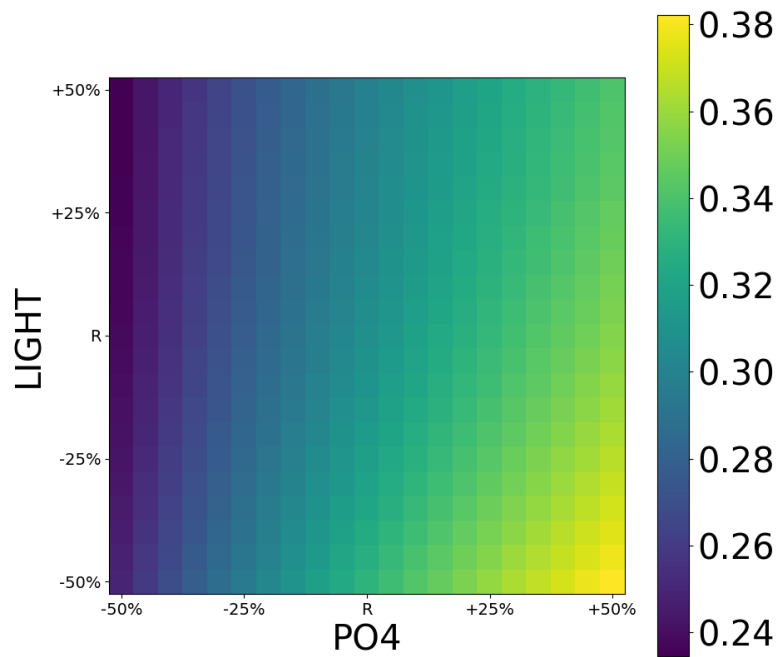
Figure S7: Sensitivity analysis of DCM width perturbing LIGHT and perturbing initial conditions of PO4 [both by an uniform factor reported on axis in percentage] along the water column. 'R' marks the reference values. The BGC-Argo floats here reported are the lovbio067c (top) and the lovbio018c (bottom). Each pixel is a full simulation, for a total of 21x21 simulations. The thickness is defined as $\pm\sigma/2$ computed on the vertical profiles by means of a Gaussian fit and averaged over the simulation period.

Figure S8: Sensitivity analysis of DCM perturbing LIGHT and perturbing initial conditions of PO4 [both by an uniform factor reported on axis in percentage] along the water column. 'R' marks the reference values. The BGC-Argo floats here reported are the lovbio067c (top) and the lovbio018c (bottom). Each pixel is a full simulation, for a total of 21x21 simulations. The DCM concentration is averaged over the productive layer defined as $\pm\sigma/2$ computed on the vertical profiles by means of a Gaussian fit and averaged over the simulation period.

5 References

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